

Estimates of Genetic Parameters for Body Weight and Carcass Composition in Pekin Ducks

^{1,2,3}T.S. Xu, ²X.L. Liu, ¹W. Huang and ¹S.S. Hou

¹The Institute of Animal Science (IAS), Chinese Academy of Agricultural Sciences (CAAS),
100093 Beijing, China

²The College of Animal Science and Technology, Northwest A and F University,
Yangling, 712100 ShaanXi, China

³Tropical Crop Genetic Resource Research Institute,
Chinese Academy of Tropical Agricultural Sciences (CATAS), Danzhou, 571737 Hainan, China

Abstract: Traditional force feed technology produced excessive fat ducks and could not meet the wide range needs. This study studied the possibility of breeding muscular Pekin duck. Data collection was performed in an experimental Pekin duck line. At 7 weeks of age, 1,985 ducks were selected according to their pedigree to measure the traits studied in this study. Single and multiple trait analyses were used to estimate heritability and variance components by restricted maximum likelihood. Heritability estimation of Body Weight (BW), Keel Length (KL), Breast Breadth (BB) and Breast Meat Thickness (BMT) were moderate to high (0.20-0.53). The heritability for Breast Muscle Weight (BMW) and Breast Meat Percentage (BMP) were 0.50 and 0.47, respectively suggesting an increase of breast meat development could be achieved by selection. The heritability of Abdominal Fat Weight (AFW), Abdominal Fat Percentage (AFP), Leg Muscle Weight (LMW) and Leg Muscle Percentage (LMP) were 0.23, 0.32, 0.38 and 0.16, respectively. The genetic correlation between BW and those of BMW and BMP were 0.74 and 0.25. Which suggest that BMP, not BMW may be a selection criterion for muscular Pekin duck. The genetic correlation between BMP and those of KL, BB and BMT were 0.69, 0.69 and 0.71, respectively. The genetic correlation between BMP and AFP was -0.03, therefore body size traits could be used as the selection index for improving the BMP and selecting for higher BMP should not decrease the leanness. In conclusion, higher BMP and lower AFP Pekin duck could be achieved.

Key words: Pekin duck, genetic parameter, body weight, body size, carcass composition, correlation

INTRODUCTION

Pekin duck had been reared by Chinese farmers for as long as 200 years. In Peking, the Peking roasted duck was well known and was served in many restaurants. Most farmers and industries reared Pekin duck using a force feed technology which led to wholesome ducks. However, this feeding technology produced ducks that became fat.

This led to the possibility that Pekin duck may be strategically bred to favor muscular traits. To study this we established an experimental Pekin duck line maintained as a small-sized strain at the Waterfowl Research Center of the Institute of Animal Science of Chinese Academy of Agriculture Science. Mild selection pressure was applied for individual phenotypic values of breast meat yield/ratio

and abdominal fat yield/ratio using ducks at 7 weeks of age. Body weight of birds is one of most important traits that breeders consider for a genetic improvement program. This is due to a number of reasons. First, body weight is easily measured.

Second, it can be correlated with a number of other meat performance traits. However, the genetic background of body weight is complex. Body weight may be determined by direct genetic and maternal effects (Bihan-Duval *et al.*, 2001; Koerhuis and Thompson, 1997; Velleman *et al.*, 2003) as well as environmental factors. The maternal body weight can affect the development of a bird embryo (Koerhuis *et al.*, 1997; Hartmann *et al.*, 2003). Moreover, direct and maternal genetic effects are negatively correlated which can lead to some selection consequences (Robinson, 2003).

Genetic variability of Body Weight (BW) and body composition can influence carcass composition. Previous studies demonstrate that body composition can be significantly improved by selection with levels of breast muscle heritability ranging from 0.53-0.65 (Vereijken, 1992; Le Bihan-Duval *et al.*, 1998, 1999; Rance *et al.*, 2002).

It has been shown that the abdominal fat pad is one of the primary regions of fat deposition in chicken and directly related to total fat carcass (Griffiths *et al.*, 1978; Becker *et al.*, 1981). With the increased demand for lean meat by consumers, it is necessary to pay more attention toward fat content in duck meat and fat deposition must be discarded which may increase production costs. Leenstra and Pit (1987) suggest that animal breeding programs should search for ways to reduce carcass lipid content which may be possible by selecting against abdominal fat deposition.

Estimation of heritability and genetic correlation coefficients for such traits were primordial to the establishment of strategies to be used in animal breeding programs. Using these parameters, the evaluation of responses to selection for a trait and genetic associations among traits became possible. At the same time, constantly monitoring of these parameters in a selection program was also required. In this study, it estimate the heritability and the genetic correlation for body weight and body size and carcass composition traits in an experimental Pekin duck line.

MATERIALS AND METHODS

Data collection: Data collection was performed in the experimental Pekin duck line. For the parental generation of this line, one male duck was paired with five female ducks. No pedigree was observed at three generations. The parental generation eggs were collected for hatching and the offsprings were raised in a large group, free access to food and water. At 7 weeks of age, experimental ducks were selected according to their pedigree and the traits which were used in this study were measured. Slaughter experiment conducted 10 times and slaughtered a total of 1,985 ducks.

Body Weights (BW) were measured on live birds after 12 h without access to feed and prior to transport of birds for processing. Before slaughtering, Keel Length (KL) and Bosom Breadth (BB) were measured using a vernier caliper (precision = 0.01 cm). After slaughtering, Carcass Weight (CW), Abdominal Fat Weight (AFW), Breast Meat Thickness (BMT), Breast Muscle Weight (BMW) and Leg Muscle Weight (LMW) were measured. The ratios of BMW, LMW and AFW to CW were

calculated as Breast Meat Percentage (BMP), Leg Muscle Percentage (LMP) and Abdominal Fat Percentage (AFP).

The CW was measured on chilled carcasses after removal of feathers, head, lungs, liver, kidneys, gastrointestinal tract and abdominal fat. The weight traits were measured using an electronic balance (precision = 0.1 g). All traits were measured at 7 weeks of age. The records, animals, sires, dams, grandfathers and grandmothers used in this study were 2,535, 1,985 (965 males, 1,020 females), 120, 230, 80 and 120, respectively.

Statistical analysis: Descriptive statistics were calculated by PROC MEANS using SAS (2001). (Co) variance component estimates and genetic parameters were obtained by restricted maximum likelihood using the animal model and MTDFREEM software (Boldman *et al.*, 1993). The mathematical model used in one trait analysis was:

$$y = X\beta + Z_a a + Z_m m + e$$

Where:

- y = The dependent variables vector
- X = The fixed effects incidence matrix, associating elements from β -y
- β = The fixed effects vector
- Z_a = The random additive effects incidence matrix, associating elements from a-y
- a = The genetic value random effects vector
- Z_m = The random maternal additive effects incidence matrix, associating elements from m-y
- m = The maternal genetic value random effects vector
- e = The residual effects vector

The mathematical model used in the 2-trait analysis is as follow where y_1 and y_2 represent different traits:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_{a1} & 0 \\ 0 & Z_{a2} \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} Z_{m1} & 0 \\ 0 & Z_{m2} \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

The vectors of fixed effects for trait 1 (β_1) and trait 2 (β_2) are the same as described in the univariate model. The vectors a_1 and a_2 are random additive genetic effects and e_1 and e_2 are residual effects for trait 1 and trait 2, respectively.

The incidence matrices X_1 and X_2 associate elements of β_1, β_2 with the records in y_1 and y_2 . The incidence matrices Z_{a1} and Z_{a2} associate elements of a_1 and a_2 with the records in y_1 and y_2 . The expectation of y_1 is $X_1\beta_1$ and the expectation of y_2 is $X_2\beta_2$; the variance-covariance structure of random effects of the bivariate animal model is as the follow:

$$V \begin{bmatrix} a_1 \\ a_2 \\ m_1 \\ m_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a_1}^2 & A\sigma_{a_1a_2} & 0 & 0 & 0 & 0 \\ A\sigma_{a_2a_1} & A\sigma_{a_2}^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & M\sigma_{m_1}^2 & M\sigma_{m_1m_2} & 0 & 0 \\ 0 & 0 & M\sigma_{m_1m_2} & M\sigma_{m_2}^2 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_{e_1}^2 & I\sigma_{e_1e_2} \\ 0 & 0 & 0 & 0 & I\sigma_{e_2e_1} & I\sigma_{e_2}^2 \end{bmatrix}$$

Where:

- $\sigma_{a_1}^2$ and $\sigma_{a_2}^2$ = The direct additive genetic variances
- $\sigma_{m_1}^2$ and $\sigma_{m_2}^2$ = The maternal additive genetic variances
- $\sigma_{e_1}^2$ and $\sigma_{e_2}^2$ = The residual variances for trait 1 and 2
- $\sigma_{a_1a_2}$ = The direct genetic covariance between traits 1 and 2
- $\sigma_{m_1m_2}$ = The maternal genetic covariance between traits 1 and 2
- $\sigma_{e_1e_2}$ = The residual covariance

Because the birds were from the same experimental Pekin duck line and were raised in the same duck farming. Slaughter batch and sex was considered as the fixed effects. The random effect considered was the direct additive genetic effect and maternal genetic effect.

RESULTS AND DISCUSSION

The descriptive parameters of the traits studied in this study are shown in Table 1. Table 1 show the variance components and heritability estimated in Pekin duck. High heritability was found in BW7 (0.53). These estimations were in agreement with the estimates reported (Rance *et al.*, 2002; Le Bihan-Duval *et al.*, 1999; Malik *et al.*, 1997; Leenstra and Pit, 1987; Hu *et al.*, 1998; Lariviere *et al.*, 2009; Chen *et al.*, 2008) but higher than the observed by Lariviere *et al.* (2009). The estimated values

ranged from 0.38-0.85. The heritability estimations for KL, BB and BMT were moderate to high (0.22, 0.20 and 0.45, respectively) which diverged from the observed (Malik *et al.*, 1997). Based on the estimated heritability values of BW7, KL, BB and BMT it observed that direct selection may be effective in improving these traits.

The heritability estimates of BMW and BMP (0.50 and 0.47, respectively) were similar to the heritability reported (Le Bihan-Duval *et al.*, 1999; Lariviere *et al.*, 2009) but diverged from the observed by Gaya *et al.* (2006). These observations indicate that an increase of BMW and BMP could be achieved by direct selection. The heritability estimates of AFW and AFP (0.23 and 0.32, respectively) were different from previously published values for broiler chickens (Le Bihan-Duval *et al.*, 1999; Hu *et al.*, 1998; Lariviere *et al.*, 2009). The heritability estimates of LMW and LMP (0.38 and 0.16, respectively) were close to previously published estimates for broiler chicken (Chapuis *et al.*, 1996).

According to the review of (Chambers, 1990), the maternal effects on BW could be expected and Chapuis *et al.* (1996) estimated the size of maternal effects between 2.0 and 8.0% of total variability. In the study, the values showed a wide variation. The maternal genetic heritability for BW7, KL, BB and CW were moderate (close-0.20) whereas other traits were low in ranged (0.01-0.05). The results are similar to those of goose as studied by Szwaczkowski *et al.* (2007).

The genetic and phenotypic correlation among body weight, body size and carcass composition traits in Pekin duck are shown in Table 2. The differences between genetic and phenotypic correlations among the body weight, body size and carcass composition traits in Pekin duck are highly varied. This may suggest that environmental conditions may influence these traits acutely.

Table 1: Estimates of the variance components and heritability of the trails studied in this study (n = 1,985)

Traits	$\bar{X} \pm SD$	σ_a^2	σ_m^2	σ_{am}	σ_e^2	σ_p^2	h_a^2	h_m^2	r_{am}
BW/g	2,290.25±445.02	104,962.68	31,686.85	-55,451.98	116,845.25	198,042.80	0.53	0.16	-0.28
KL/cm	11.94±1.1000	0.26	0.22	0.06	0.66	1.20	0.22	0.18	0.05
BB/cm	11.03±0.9100	0.16	0.15	0.02	0.46	0.80	0.20	0.19	0.03
BMT/cm	1.41±0.2000	0.02	0.00	-0.01	0.03	0.04	0.45	0.05	-0.14
CW/g	1,843.81±159.32	13,199.11	3,045.95	-4315.09	13,452.94	25,382.90	0.52	0.12	-0.17
BMW/g	158.70±29.080	422.80	42.28	-118.38	498.90	845.60	0.50	0.05	-0.14
LMW/g	119.96±13.710	71.44	1.88	-22.56	137.24	188.00	0.38	0.01	-0.12
AFW/g	37.63±8.8400	17.96	0.78	-1.56	60.92	78.10	0.23	0.01	-0.02
BMP/%	8.60±1.3200	0.80	0.02	-0.09	0.97	1.70	0.47	0.01	-0.05
LMP/%	13.04±1.2500	0.26	0.03	-0.02	1.33	1.60	0.16	0.02	-0.01
AFP%	2.06±0.5100	0.10	0.01	-0.02	0.21	0.30	0.32	0.03	-0.06

BW = Body Weights, KL = Keel Length, BB = Bosom Breadth, BMT = Breast Meat Thickness, CW = Carcass Weight, BMW = Breast Muscle Weight, LMW = Leg Muscle Weight, AFW = Abdominal Fat Weight, BMP = Breast Meat Percentage, LMP = Leg Muscle Percentage, AFP = Abdominal Fat Percentage, σ_a^2 is additive direct genetic variance, σ_m^2 is additive maternal genetic variance, σ_{am} is genetic covariance between direct and maternal genetic effects, σ_e^2 is residual variance and σ_p^2 is the phenotypic variance. h_a^2 is additive heritability (σ_a^2/σ_p^2); h_m^2 is heritability for maternal effect (σ_m^2/σ_p^2); r_{am} is the correlation between additive effect and maternal effect ($\sigma_{am}^2/\sigma_{am}$)

Table 2: Genetic correlation (below the diagonal and phenotypic correlation (above the diagonal estimated from body weight, body size and carcass composition traits in this study

Traits	BW7	KL	BB	BMT	CW	BMW	LMW	AFW	BMP	LMP	AFP
BW7		0.43	0.42	0.27	0.37	0.21	0.21	0.16	0.03	-0.09	0.04
KL	0.73		0.84	0.62	0.33	0.36	0.15	0.19	0.24	-0.12	0.07
BB	0.63	0.77		0.63	0.25	0.26	0.19	0.11	0.16	0.00	0.03
BMT	0.57	0.70	0.72		0.39	0.40	0.19	0.16	0.25	-0.12	0.07
CW	0.85	0.66	0.60	0.62		0.52	0.55	0.38	0.07	-0.25	0.06
BMW	0.74	0.73	0.70	0.72	0.69		0.19	0.30	0.88	-0.23	0.11
LMW	0.48	0.26	0.30	0.28	0.58	0.28		0.16	-0.06	0.66	0.03
AFW	0.18	0.03	-0.01	0.01	0.13	0.24	0.11		0.15	-0.15	0.83
BMP	0.25	0.69	0.69	0.71	0.44	0.91	0.10	0.23		-0.12	0.10
LMP	-0.38	-0.52	-0.38	-0.74	-0.40	-0.47	0.44	0.03	-0.48		-0.02
AFP	-0.04	-0.18	-0.16	-0.13	-0.14	0.04	-0.03	0.89	0.09	0.18	

The genetic correlation between BW and BMW, BMP were 0.74, 0.25, respectively. Previous studies estimated the genetic correlation between BMW, BMP and BW and analyzed the relationship of BMW and BW, BMP and AFP and BW and Intramuscular Fat Percentage (IFP) (Le Bihan-Duval *et al.*, 1998, 1999). However, these studies did not indicate which trait was used as the most advisable index for selecting muscular poultry. Because BW and BMW are genetically correlative, adding breast weight to selection offers no advantage over body weight alone (Cahaner and Nitsan, 1985). However, the situation is different when the percentage of Breast Meat Weight (BMP) is considered because the latter is poorly correlated with body weight as indicated in the present study (0.25). Moreover, the results show the heritability of BMP was high (0.47). Therefore, BMP can be used as an advisable selection criterion for selecting muscular Pekin duck. However, obtaining measurements of BMP in live Pekin duck is difficult. This may resort to the high genetic correlation observed between BMP and KL, BB, BMT (0.69, 0.69 and 0.71, respectively) presented in this study. So the BMT alone or the synthetic selection index using KL, BB and BMT which were measured in live Pekin duck could be used as the selection index for improving the BMP.

It observed a slight negative correlation between BMP and AFP (-0.03). As a result, selecting for higher BMP should not decrease the leanness of birds. This is consistent with the results of experimental selection of chickens for lower abdomen fat that had higher breast meat percentages than for higher abdominal fat (Cahaner *et al.*, 1986) or higher body weight (Leenstra, 1981). Moreover, selecting for meat-type birds may indirectly cause leg deformities. Abourachid (1993) observed from a biomechanical study in Turkey that femurs of meat-type birds were more bent than those of traditional birds. In chicken, a moderate unfavorable genetic correlation was found between susceptibility to varus deformity and breast angle or breast meat percentage (Le Bihan-Duval *et al.*, 1997). Improving breast meat percentage would cause what consequences? Additional studies are needed to study the impact. The

results of the study show that the genetic correlation estimated between BMW and LMW (0.28) and was positive. However, it is not possible to select for higher BWP and higher LMP in Pekin duck because of the high negative genetic correlation (-0.48) between BWP and LMP.

CONCLUSION

The study suggests that direct selection would be effective in improving body size traits as determined by the heritability estimates. The heritability estimates for BMW and BMP (0.50 and 0.47, respectively) indicate that an appreciable increase of breast meat development could be achieved by direct selection. The maternal genetic heritability of BW7, KL, BB and CW were moderate (close-0.20) whereas the maternal genetic heritability of the other traits in this study ranged from 0.01-0.05. Higher BMP and lower AFW Pekin duck could be achieved by selecting using body size traits. Moreover, the BMP could be improved using body size traits as the indirect selection index or comprehensive selection index in live Pekin duck.

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